

PCT
09

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/787,633

DATE: 03/28/2001
 TIME: 17:45:04

Input Set : A:\seqlist.txt
 Output Set: N:\CRF3\03282001\I787633.raw

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3 <110> APPLICANT: Wilson, Robert JM
 4 Mullineaux, Conrad W
 5 Law, Anna E
 7 <120> TITLE OF INVENTION: Treatment of Infection
 9 <130> FILE REFERENCE: 117-347
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/787,633
 12 <141> CURRENT FILING DATE: 2001-03-21
 14 <150> PRIOR APPLICATION NUMBER: PCT/GB99/03180
 15 <151> PRIOR FILING DATE: 1999-09-22
 17 <150> PRIOR APPLICATION NUMBER: GB 9820658.4
 18 <151> PRIOR FILING DATE: 1998-09-22
 20 <160> NUMBER OF SEQ ID NOS: 7
 22 <170> SOFTWARE: PatentIn Ver. 2.1
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 1444
 26 <212> TYPE: DNA
 27 <213> ORGANISM: Plasmodium falciparum
 29 <220> FEATURE:
 30 <221> NAME/KEY: CDS
 31 <222> LOCATION: (26)..(1435)
 33 <220> FEATURE:
 34 <221> NAME/KEY: misc_feature
 35 <222> LOCATION: (1276)
 36 <223> OTHER INFORMATION: h represents A, T or C
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 41 1 5
 43 att tat aat tta aat tat aaa tat caa tat aaa aat aaa ata aat tta 100
 44 Ile Tyr Asn Leu Asn Tyr Lys Tyr Gln Tyr Lys Asn Lys Ile Asn Leu
 45 10 15 20 25
 47 tat tta ata aga caa gga tta aat ata aat tta ata aaa aat tta tct 148
 48 Tyr Leu Ile Arg Gln Gly Leu Asn Ile Asn Leu Ile Lys Asn Leu Ser
 49 30 35 40
 51 agt aat att ttt tta tat atg ttt att tat aat ttt aaa aaa tat tct 196
 52 Ser Asn Ile Phe Leu Tyr Met Phe Ile Tyr Asn Phe Lys Lys Tyr Ser
 53 45 50 55
 55 tta aaa tta tta aat ata ttt aaa tta cct gat tgg aat ttt ttt gat 244
 56 Leu Lys Leu Leu Asn Ile Phe Lys Leu Pro Asp Trp Asn Phe Phe Asp
 57 60 65 70
 59 tgt cca aat ata aat tat gat aat att att tat tat tct tct att tta 292
 60 Cys Pro Asn Ile Asn Tyr Asp Asn Ile Ile Tyr Tyr Ser Ser Ile Leu
 61 75 80 85
 63 aaa gat aat aat tta ata tat tat tta aaa aat aat tta aat att gaa 340
 64 Lys Asp Asn Asn Leu Ile Tyr Tyr Leu Lys Asn Asn Leu Asn Ile Glu
 65 90 95 100 105
 67 ttt tta gat agt ata tta ata aaa aat aat tct ata gat att ata ttt 388

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OK
W-->

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68 Phe Leu Asp Ser Ile Leu Ile Lys Asn Asn Ser Ile Asp Ile Ile Phe
69      110      115      120
71 gat agt atg tct att tta cat act aca caa tat ttt tta aaa aaa tth 436
72 Asp Ser Met Ser Ile Leu His Thr Thr Gln Tyr Phe Leu Lys Lys Xaa
73      125      130      135
75 gga ata att ttt tta cct tta ttt gat att ata ttt aaa tat cct tta 484
76 Gly Ile Ile Phe Leu Pro Leu Phe Asp Ile Ile Phe Lys Tyr Pro Leu
77      140      145      150
79 tta ata aaa aaa tat tta ggt act att att tct tat aaa gat aat ttt 532
80 Leu Ile Lys Lys Tyr Leu Gly Thr Ile Ile Ser Tyr Lys Asp Asn Phe
81      155      160      165
83 ttt gct aat att aat tca ata ata ttt agt gaa gga tct ttt tgt tat 580
84 Phe Ala Asn Ile Asn Ser Ile Ile Phe Ser Glu Gly Ser Phe Cys Tyr
85 170      175      180      185
87 ata cct aaa tat gta aag tgt aat ttt aat tta tca aca tat ttt aaa 628
88 Ile Pro Lys Tyr Val Lys Cys Asn Phe Asn Leu Ser Thr Tyr Phe Lys
89      190      195      200
91 act aat tct tct gat ttt gca caa ttt gaa cgt act tta ata ata gtt 676
92 Thr Asn Ser Ser Asp Phe Ala Gln Phe Glu Arg Thr Leu Ile Ile Val
93      205      210      215
95 ggt aaa tat tct tat gta tca tat tta gaa gga tgt aca gct tca tta 724
96 Gly Lys Tyr Ser Tyr Val Ser Tyr Leu Glu Gly Cys Thr Ala Ser Leu
97      220      225      230
99 tat aaa gaa tca caa tta cat gta gct ata gta gaa ata ata gta aaa 772
100 Tyr Lys Glu Ser Gln Leu His Val Ala Ile Val Glu Ile Ile Val Lys
101      235      240      245
103 gat tat ggt tat ata aaa tat tat aca tta caa aat tgg tat aga gga 820
104 Asp Tyr Gly Tyr Ile Lys Tyr Tyr Thr Leu Gln Asn Trp Tyr Arg Gly
105 250      255      260      265
107 gat tat tta ggt aat ggt ggt tta tat aat ttt aca act aaa cgt ggt 868
108 Asp Tyr Leu Gly Asn Gly Gly Leu Tyr Asn Phe Thr Thr Lys Arg Gly
109      270      275      280
111 ata tgt tta aat tat tca aaa tta gat tgg ata caa gtt gaa gta ggt 916
112 Ile Cys Leu Asn Tyr Ser Lys Leu Asp Trp Ile Gln Val Glu Val Gly
113      285      290      295
115 tcg att ata aca tgg aaa tac cct tct act att tta aaa ggt aaa ttt 964
116 Ser Ile Ile Thr Trp Lys Tyr Pro Ser Thr Ile Leu Lys Gly Lys Phe
117      300      305      310
119 tct att agt aat ttt tat tca ata tct ttt ata tca aat atg caa ata 1012
120 Ser Ile Ser Asn Phe Tyr Ser Ile Ser Phe Ile Ser Asn Met Gln Ile
121      315      320      325
123 gct gat act ggt agt aaa atg tat cat ata gga tct tat act aaa agt 1060
124 Ala Asp Thr Gly Ser Lys Met Tyr His Ile Gly Ser Tyr Thr Lys Ser
125 330      335      340      345
127 tat ata att tct aaa agt ata tct tta aat aac tca tta aat ata ttt 1108
128 Tyr Ile Ile Ser Lys Ser Ile Ser Leu Asn Asn Ser Leu Asn Ile Phe
129      350      355      360
131 aga ggt tta gta tat att aaa cct ttt tca tat aaa tct tat aat tat 1156
132 Arg Gly Leu Val Tyr Ile Lys Pro Phe Ser Tyr Lys Ser Tyr Asn Tyr

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135 act gaa tgt agt tct tta ata ttt ggt aat aat tct tta aca gta act 1204
136 Thr Glu Cys Ser Ser Leu Ile Phe Gly Asn Asn Ser Leu Thr Val Thr
137          380          385          390
139 att cct tat ata aaa aat tat aat aat act agt tat gta aaa caa gaa 1252
140 Ile Pro Tyr Ile Lys Asn Tyr Asn Asn Thr Ser Tyr Val Lys Gln Glu
141          395          400          405
143 gct ttt gtt tct aaa att gaa ath ata tat tta ttt tta tta atg caa 1300
144 Ala Phe Val Ser Lys Ile Glu Ile Ile Tyr Leu Phe Leu Leu Met Gln
145 410          415          420          425
147 cgt ggt tta agt att tca gag tct att tca tta tta att ata ggt ttt 1348
148 Arg Gly Leu Ser Ile Ser Glu Ser Ile Ser Leu Leu Ile Ile Gly Phe
149          430          435          440
151 tgt tct gat att tat aat aaa tta ccg ttt gaa ttt aat tta gag ata 1396
152 Cys Ser Asp Ile Tyr Asn Lys Leu Pro Phe Glu Phe Asn Leu Glu Ile
153          445          450          455
155 cct ata tta ttt tca tta aaa att aaa gat ata ttt aat taattaaat 1444
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164 <213> ORGANISM: Synechocystis PCC6803
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168 <222> LOCATION: (1)..(1443)
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175 ggc ttt gtc acc aac att gaa gcg gat gct atc ccc cgt ggt ctg agt 96
176 Gly Phe Val Thr Asn Ile Glu Ala Asp Ala Ile Pro Arg Gly Leu Ser
177 20 25 30
179 gaa gac gtg gtg cga ctc att tct gct aag aaa aat gaa ccc gaa ttc 144
180 Glu Asp Val Val Arg Leu Ile Ser Ala Lys Lys Asn Glu Pro Glu Phe
181 35 40 45
183 atg ttg gat ttt cgc ctc cgg gcc tac cgg cat tgg ctg acc atg gcg 192
184 Met Leu Asp Phe Arg Leu Arg Ala Tyr Arg His Trp Leu Thr Met Ala
185 50 55 60
187 gaa ccc act tgg ccg gcg gtg cat tat ccc ccc att gat tac caa gat 240
188 Glu Pro Thr Trp Pro Ala Val His Tyr Pro Pro Ile Asp Tyr Gln Asp
189 65 70 75 80
191 att att tac tac tcc gcc cct aag caa agt aag aaa aaa cta gaa agc 288
192 Ile Ile Tyr Tyr Ser Ala Pro Lys Gln Ser Lys Lys Lys Leu Glu Ser
193 85 90 95
195 tta gat gaa gtg gac cca gct ttg ttg gaa acc ttt gaa aaa tta ggg 336
196 Leu Asp Glu Val Asp Pro Ala Leu Leu Glu Thr Phe Glu Lys Leu Gly
197 100 105 110
199 att ccc cta tcg gag caa aaa cgt tta agt aat gtg gcg gta gat gcc 384

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204 Ile Phe Asp Ser Val Ser Ile Gly Thr Thr Phe Lys Glu Lys Leu Ala
205      130          135          140
207 gaa gac ggg gta att ttc tgt tct att tct gaa gca ttg cag gaa cat 480
208 Glu Asp Gly Val Ile Phe Cys Ser Ile Ser Glu Ala Leu Gln Glu His
209 145          150          155          160
211 ccc gac ctg gtg caa aaa tat ttg ggc agt gtg gtg ccc acc gcc gac 528
212 Pro Asp Leu Val Gln Lys Tyr Leu Gly Ser Val Val Pro Thr Ala Asp
213          165          170          175
215 aac ttc ttt gcc gcc tta aac tct gct gta ttt agt gac ggt tcc ttt 576
216 Asn Phe Phe Ala Ala Leu Asn Ser Ala Val Phe Ser Asp Gly Ser Phe
217          180          185          190
219 gtt ttt att ccc aaa ggg gtg aag tgt ccc atg gaa ttg tcc acc tat 624
220 Val Phe Ile Pro Lys Gly Val Lys Cys Pro Met Glu Leu Ser Thr Tyr
221      195          200          205
223 ttc cgc att aat aat ggg gat acg ggg cag ttt gag cgg aca tta att 672
224 Phe Arg Ile Asn Asn Gly Asp Thr Gly Gln Phe Glu Arg Thr Leu Ile
225      210          215          220
227 att gcc gaa gaa ggg gct tcc gtt agc tat ttg gaa ggt tgt act gcg 720
228 Ile Ala Glu Glu Gly Ala Ser Val Ser Tyr Leu Glu Gly Cys Thr Ala
229 225          230          235          240
231 ccc atg tat gac acc aat caa ctt cat gcg gcg gtg gtg gaa ttg gta 768
232 Pro Met Tyr Asp Thr Asn Gln Leu His Ala Ala Val Val Glu Leu Val
233          245          250          255
235 gct cta gat aat gct gac att aaa tat tcc acc gta caa aac tgg tac 816
236 Ala Leu Asp Asn Ala Asp Ile Lys Tyr Ser Thr Val Gln Asn Trp Tyr
237          260          265          270
239 gct ggg gac gaa aat ggc aag ggc gga att tac aac ttt gtg act aaa 864
240 Ala Gly Asp Glu Asn Gly Lys Gly Gly Ile Tyr Asn Phe Val Thr Lys
241      275          280          285
243 cgg ggt cta tgt aaa gga gtt aat tcc aaa att tcc tgg acc caa gta 912
244 Arg Gly Leu Cys Lys Gly Val Asn Ser Lys Ile Ser Trp Thr Gln Val
245      290          295          300
247 gaa acc ggt tcc gcc att acc tgg aaa tac ccc agt tgt gtg cta gtt 960
248 Glu Thr Gly Ser Ala Ile Thr Trp Lys Tyr Pro Ser Cys Val Leu Val
249 305          310          315          320
251 ggg gat aat tcc gtc ggg gaa ttc tac tct att gct tta act aac aac 1008
252 Gly Asp Asn Ser Val Gly Glu Phe Tyr Ser Ile Ala Leu Thr Asn Asn
253          325          330          335
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257          340          345          350
259 acc cgt agt atc att att tcc aaa ggc att tcc gct ggt aat tcc gcc 1104
260 Thr Arg Ser Ile Ile Ile Ser Lys Gly Ile Ser Ala Gly Asn Ser Ala
261      355          360          365
263 aac agt tac cgg ggt ttg gtg aaa atg gga cct aaa gcc cag ggc gct 1152
264 Asn Ser Tyr Arg Gly Leu Val Lys Met Gly Pro Lys Ala Gln Gly Ala

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265      370      375      380
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271 gct aat act ttt ccc tat att caa gtg gac aat aat acc gcc aaa gta 1248
272 Ala Asn Thr Phe Pro Tyr Ile Gln Val Asp Asn Asn Thr Ala Lys Val
273      405      410      415
275 gaa cat gaa gct tcc act tcc aaa att ggc gag gat caa ctc ttt tac 1296
276 Glu His Glu Ala Ser Thr Ser Lys Ile Gly Glu Asp Gln Leu Phe Tyr
277      420      425      430
279 ttt gcc caa cgg gga att tct gag gaa gat gcg gtg tcc atg cta gtc 1344
280 Phe Ala Gln Arg Gly Ile Ser Glu Glu Asp Ala Val Ser Met Leu Val
281      435      440      445
283 agc ggt ttc tgt aag gat gtg cta aac gaa tta ccc atg gaa ttt gcg 1392
284 Ser Gly Phe Cys Lys Asp Val Leu Asn Glu Leu Pro Met Glu Phe Ala
285      450      455      460
287 gcg gag gct gat aaa tta ctg agt ctc aaa cta gaa ggt act gtg ggt 1440
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298 <213> ORGANISM: Escherichia coli
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309 aat act gaa gca act gac gat gtc aaa acc tgg acc ggc ggc ccg ctg 96
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311 20 25 30
313 aat tat aaa gaa gga ttc ttc acc cag tta gcc acc gat gag ctg gca 144
314 Asn Tyr Lys Glu Gly Phe Phe Thr Gln Leu Ala Thr Asp Glu Leu Ala
315 35 40 45
317 aag ggg ata aac gaa gag gtg gtg cgc gca att tcg gcg aag cgt aat 192
318 Lys Gly Ile Asn Glu Glu Val Val Arg Ala Ile Ser Ala Lys Arg Asn
319 50 55 60
321 gag ccg gag tgg atg ctg gag ttt cgt cta aac gcc tat cgc gca tgg 240
322 Glu Pro Glu Trp Met Leu Glu Phe Arg Leu Asn Ala Tyr Arg Ala Trp
323 65 70 75 80
325 ctg gag atg gaa gaa ccg cac tgg ttg aaa gcg cac tac gac aag ctg 288
326 Leu Glu Met Glu Glu Pro His Trp Leu Lys Ala His Tyr Asp Lys Leu
327 85 90 95
329 aat tat cag gat tac agc tac tac tca gca cca tcg tgc ggt aat tgt 336
330 Asn Tyr Gln Asp Tyr Ser Tyr Tyr Ser Ala Pro Ser Cys Gly Asn Cys
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VERIFICATION SUMMARY

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L:72 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1